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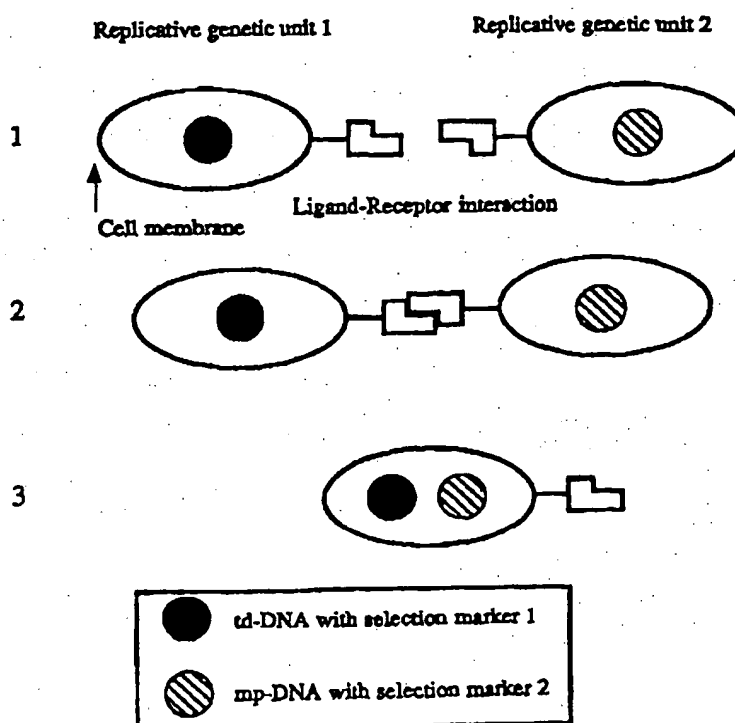
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(71) Applicant (for all designated States except US): BIOINVENT INTERNATIONAL AB [SE/SE]; S-223 70 Lund (SE).			
(71) Applicant (for MN only): KIDDLE, Simon, John [GB/GB]; Mewburn Ellis, York House, 23 Kingsway, London WC2B 6HP (GB).			
(72) Inventors; and (75) Inventors/Applicants (for US only): BORREBAECK, Carl [SE/SE]; Årtevägen 8 A, S-245 62 Hjärrup (SE). MALMBORG, Anki [SE/SE]; Tullgatan 3 A, S-223 54 Lund (SE). SÖDERLIND, Eskil [SE/SE]; Qvantenborgsvägen 23, S-227 38 Lund (SE).			
(74) Agents: KIDDLE, Simon, John et al.; Mewburn Ellis, York House, 23 Kingsway, London WC2B 6HP (GB).			

(54) Title: COMBINED LIGAND AND RECEPTOR DISPLAY

(57) Abstract

A method for selecting nucleic acid sequences encoding ligand and receptor molecules capable of specific binding to each other is disclosed in which nucleic acid encoding ligand or receptor molecules is expressed in a host microorganism in combination with a surface molecule, such as *E. coli pili*, so that the ligand or receptor are displayed on the surface of the host microorganism. A replicable genetic unit, such as a filamentous bacteriophage, is used to display candidate binding partners to the ligand or receptor, with the binding of the ligand or receptor to the candidate binding partner mediating the transfer of nucleic acid from the replicable genetic unit to the microorganism. The method can be highly selective as the host microorganism is modified so that it does not display the surface molecule other than as a fusion with the ligand or receptor molecule. The method is rapid and simple and opens up new applications based on the detection of ligand and receptors where both are unknown.



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Combined Ligand and Receptor Display

Field of the Invention

5 The present invention relates to methods for selecting specific ligand and receptor encoding sequences and to kits for carrying out the methods.

Background of the Invention

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There is a continuing need for highly efficient selection systems in the screening of protein libraries, such as antibody libraries. Current systems are based on the display of antibodies on the surface of microorganisms
15 containing the gene of the antibody. Specific clones can then be selected with immobilized antigens, for instance by panning on microtiter plates (Parmley and Smith, 1988, Gene, 73, 305-318 and Barbas III et al, 1991, PNAS 88, 7978-7982), selection on magnetic beads (Hawkins et al,
20 1992, J. Mol. Biol. 226, 889-896), immunotubes (Marks et al, 1991, J. Mol. Biol, 222, 581-597), affinity chromatography (McCafferty et al, 1990, Nature, 348, 552-554), fluorescence assisted cell sorter (FACS), antigen specific precipitation (Kang et al, 1991, PNAS, 88, 4363-
25 4366) and SAP (Dueñas and Borrebaeck, 1994, Bio/Technology 12, 999-1002).

Several antibody libraries have been constructed on the surface of phages, e.g. a bacteriophage such as fd
30 (McCafferty et al, 1990, Nature, 348, 552-554) or M13 (Barbas III et al, 1991, PNAS, 88, 7978-7982). The possibility of expressing antibodies (scFv) on the surface of bacteria has also been demonstrated by fusions to bacterial membrane proteins like Lpp-Omp A (Francisco et al,
35 1993, PNAS, 90, 10444-10448) and PAL (Fuchs et al, 1991, Bio/Technology, 9, 1369-1372). For a recent review of antibody display systems and the screening of antibody libraries, see Little, 1994, Biotech. Adv., 12, 539-555.

Antigen libraries have been constructed following essentially the same principles as antibody libraries, e.g. peptide libraries on the surface of bacteriophages (Smith, 1985, Science, 228, 1315-1317). Expression of antigens on the surface of bacteria has been demonstrated by fusions to LamB (Charbit et al, 1988, Gene, 70, 181-189 and Bradbury et al, 1993, Bio/Technology, 1565-1568), Omp A (Pistor and Hoborn, 1989, Klin. Wochenschr., 66, 110-116), fimbriae (Hedegaard and Klemm, 1989, Gene, 85, 115-124 and Hofnung, 1991, Methods Cell Biol., 34, 77-105), IgA protease β domain (Klauser et al, 1990, EMBO J., 9, 1991-1999) and flagellae (Newton et al, 1989, Science, 244, 70-72).

However, many of the prior art selection steps, such as panning and affinity chromatography, are not very efficient, and even if the yield of antibody or antigen is reasonable, these techniques do not provide any information about the nucleic acid sequence encoding it.

Summary of the Invention

In the past, it has not been possible to combine a ligand library with a receptor library in order not only to clone and select one of the specific binding pair members and their corresponding nucleic acid sequences encoding them, but actually both.

The present invention provides an efficient screening technique to obtain corresponding ligand/receptor molecules and establishes a physical and logical connection between the two and their encoding sequences. This has the advantage that it is simple and rapid and opens up possibilities of applications, such as detecting new ligands and/or receptors, where both are unknown, as well as improvements regarding epitope mapping, localization of gene products and drug design.

Accordingly, in one aspect, the present invention provides a method for selecting nucleic acid sequences encoding ligand and receptor molecules capable of specific binding to each other, the method comprising:

(a) expressing in a host microorganism nucleic acid encoding a surface molecule which is operably linked to the expression of nucleic acid encoding a ligand or receptor molecule, or a functional fragments thereof, so that the microorganism expresses the surface molecule and the ligand or receptor molecule as a fusion and displays it on its surface, wherein the host microorganism is modified so that it does not display the surface molecule other than as a fusion with the ligand or receptor molecule;

(b) contacting the modified host microorganism of step (a) with one or more replicable genetic units capable of expressing nucleic acid encoding ligand or receptor molecules, or functional fragments thereof, the ligand or receptor molecules being candidates for specific binding to the molecules displayed by the host microorganisms of step (a) and being expressed as fusions with a surface protein of the replicable genetic unit, wherein binding of the surface displayed ligand and receptor molecules mediates the transfer of the nucleic acid encoding the ligand or receptor from the replicable genetic unit to the microorganism; and,

(c) selecting the host microorganisms containing the nucleic acid sequences encoding the ligand and receptor molecules, or functional fragments thereof.

Thus, in this aspect, the invention provides a method for selecting nucleic acid sequences encoding ligand and receptor molecules, the selection arising from modification to the host microorganism so that infection or transfer of the nucleic acid from the replicable genetic unit takes place when binding of the receptor and ligand molecules occurs. Thus, infection via the normal route, e.g. for E.

coli via wild type pili, is prevented by a modification to the host microorganism to prevent the display of a given type of surface molecule so that the only surface molecules of that type that are displayed are those fused to the receptor or ligand.

In a preferred aspect, the host microorganism expresses and displays modified ligand molecules, with the replicable genetic units expressing the candidate receptor molecules. Thus, this provides a method for selecting specific ligand and receptor encoding sequences wherein:

(a) the expression of a surface molecule encoding sequence is combined with a ligand encoding sequence, or a sequence encoding a functional fragment thereof, so that the host microorganism expresses modified ligand molecules on its surface;

(b) infecting, or in other ways transferring DNA to, the modified host organism of step (a) with a genetically modified replicable genetic unit capable of expressing a receptor, or a functional fragment thereof, fused to a surface protein of the replicable genetic unit; and,

(c) selecting infected host organisms containing specific ligand and receptor encoding sequences or sequences encoding functional fragments thereof.

In the above aspects, the method of the invention optionally includes the additional step of:

(d) isolating the nucleic acid sequences encoding the ligand or receptor molecules.

Conveniently, the isolation can be achieved by associating different selection markers (e.g. different antibiotic resistance markers) with the nucleic acid sequences encoding the ligand and receptor molecules. Thus, the host microorganisms containing nucleic acid sequences encoding a specific binding pair can be selected by growing them in

the presence of both antibiotics. After this, the vectors containing nucleic acid encoding the ligand and the receptor can be separated from each other by omitting one of the antibiotics from the growing medium.

In different embodiments, this method can be used to screen:

- (a) microorganisms displaying one type of ligand or receptor molecule against libraries of replicable genetic units displaying different receptor or ligand molecules;
- (b) libraries of microorganisms displaying different ligand or receptor molecules against replicable genetic units displaying one type of receptor or ligand molecule;
- or,
- (c) libraries of microorganisms displaying different ligand or receptor molecules against libraries of replicable genetic units displaying different receptor or ligand molecules.

In the above aspects, the host microorganisms do not express the normal (wild type) surface molecules that are used to display ligand or receptor molecules as fusions on its surface. This means that the replicable genetic units used to display candidate binding partners of the ligand or receptor molecule will only infect the microorganisms when binding between the ligand or receptor and a binding partner takes place, i.e. infection via the normal surface molecule of the microorganism is not possible as they are not displayed.

Thus, in one embodiment, the host microorganism is an E. coli strain in which the F episome is mutated in the traA gene that builds up pilin molecules, but which contains the other genes required for infection by bacteriophages, e.g. traL, traE, traY etc. Accordingly, these strains of E. coli are F', that is they do not produce functional pili,

except when transformed with vectors comprising nucleic acid encoding fusions of the pilin and the ligand or receptor molecules. This allows wild type bacteriophages (e.g. M13, fd etc) displaying the candidate binding partners attached to a phage surface protein (e.g. pIII or pVIII protein) to be used, as the bacteriophage will only selectively infect those E. coli cells binding to the phage via the specific interaction of the binding partners. As the E. coli do not have wild type pili, this prevents the bacteriophage infecting the E. coli unselectively. Thus, the present invention does not rely on engineering the replicable genetic units to limit their infectivity, and so obtain selectivity of DNA transfer, helping to avoid the difficulties that can be encountered in generating large libraries with deleted bacteriophages, such as pIII deleted M13 phage.

In embodiments of the invention that use the pili of the microorganism to display the ligand or receptor molecules, surprisingly good selectivity is obtained when the ligand or receptor nucleic acid is expressed as a fusion at the carboxy terminus of the pili.

Preferably, the vectors comprising the nucleic acid encoding the ligand and receptor molecules have different origins of replication (pMB1, p15A, PSC101) so that both vectors can be stably maintained when transferred to the host microorganism.

In the method, steps (a) and (b) can be simultaneous or sequential. However, conveniently, the host microorganism will be cultured so that they display the ligand or receptor molecules, prior to infection with the replicable genetic units.

Accordingly, the present invention provides a method for selection of nucleic acid sequences encoding ligand and receptor molecules capable of specific binding to each other. The designed system enables the passage of DNA over cell membranes and is denoted "Cellular Linkage of ligand-receptor Affinity Pairs" (CLAP). The DNA which is translocated from the replicable genetic unit over the cell membrane is denoted "membrane passage DNA" (mp-DNA) and this genetic information outside the cell can be defined, constructed, designed and developed using recombinant DNA technology. The type of specific DNA, which is translocated over the cell membrane, is determined by the genetic information, DNA, inside the cell. This genetic information inside the cell can be defined, constructed, designed and developed using recombinant DNA technology and is denoted "translocation determining DNA" (td-DNA). Thus, in a preferred embodiment, this selectivity of DNA transfer is achieved using a strain of E. coli that have a mutation in the F episome so that they do not display functional pili. This means that when they are transformed with a vector comprising nucleic acid encoding a ligand or receptor for expression as a fusion with the pili, only these modified pili are displayed on the E. coli surface.

Based on the capability of specific td-DNA to determine the specific type of mp-DNA which is to be translocated into cells, the CLAP system can be used to construct a genetic library of td-DNA to determine the translocation of specific mp-DNA from a genetic library of mp-DNA. Thus, it is possible, in one single reaction, to mix a replicable genetic unit or units which encode genetic library/libraries of td-DNA and a genetic library/libraries of mp-DNA and these libraries encode proteins/peptides which are expressed from the genetic library/libraries. The individual td-DNA in individual cells will determine the translocation of individual mp-DNA into each cell.

Thus, the corresponding pairs of td-DNA and mp-DNA will be linked in the same cell. Individual td-DNA and mp-DNA can be separated and isolated using selection markers and
5 therefore both the td-DNA and mp-DNA from the same cell can be separated, analyzed, defined, redesigned and reconstructed. The possibility to screen two gene libraries against each other in one reaction step allows the selection of ligand-receptor pairs without information
10 of the individual clones building up the ligand-receptor pair. The td-DNA can be constituted of genes encoding proteins or peptides of various sizes. Individual cells encode specific proteins/peptides defined by the td-DNA in the cell and this protein or peptide is exposed on the cell
15 surface. These exposed proteins/peptides can be constructed as mp-DNA and displayed on the surface of a replicable genetic unit. These proteins/peptides can be viewed as receptors and can then interact with ligand molecules exposed, encoded by the td-DNA, on the cell
20 surface. When such interactions occur the ligand-receptor interaction mediates the passage of receptor DNA (mp-DNA) into the cell.

In one embodiment, the molecules on the cell surface are
25 receptors and the molecules on the replicable genetic unit are ligands. A td-DNA can consist of a cDNA-library and the mp-DNA can consist of an antibody fragment gene library, where antibody fragment specificities can be selected against different protein/peptides ligand. The
30 td-DNA can also consist of DNA encoding one type of peptide which can bind biotin and biotinylated chemical compounds. The biotin-peptide interaction allows the immobilization of biotinylated chemical compounds on the cell surface and these immobilized compounds can function as
35 ligands/receptors for determining the translocation of mp-DNA encoding receptors/ligands. Antibody fragments with affinity to the immobilized chemical compound can be

selected from a genetic library encoding different antibody specificities/affinities. The mp-DNA encoding the specificity/affinity of the selected antibody fragment is then replicated inside the cell, which displayed the biotin binding peptide binding to the biotinylated chemical compound. Other types of modifications of the chemical compounds can be used, which bind the biotin binding peptide and other types of peptides can be displayed on the cell surface which bind the modified chemical compound.

In a further aspect, the present invention provides a kit containing vectors for use in the methods described herein.

In this aspect, a preferred kit comprises:

(a) a host microorganism modified so that it does not display a wild type surface protein;

(b) a vector encoding said surface protein and having restriction sites for the insertion of nucleic acid encoding ligand or receptor molecules, or functional fragments thereof, so that when transformed into the host microorganism, the surface molecule and the ligand or receptor molecule are expressed as a fusion and displayed on the surface of the microorganism;

(c) a bacteriophage having a site for insertion of nucleic acid encoding candidate binding partners to the ligand or receptor so that the binding partners are expressed displayed on the surface of the bacteriophage as a fusion with a surface protein of the bacteriophage.

The above method can be used in a variety of applications, inter alia:

(1) cDNA libraries derived from, e.g. genome sequences, human or other tissue, can be cloned into the fusion vector and subsequently transfected into the microorganism host. Thus, by the way of expressing cDNA derived molecules as fusion proteins to pilin, we can use these cells as expressors of ligands. Subsequently,

bacteriophages displaying antibody fragments derived from immunised or naive B cells from human or other origin will be formed and allowed to interact with the host microorganism expressing cDNA derived molecules. The infection event takes place and is mediated only by specific receptor-ligand interactions found between microorganisms and bacteriophages. The genetic information for each ligand and receptor pair can then be isolated.

(2) cDNA libraries derived from cancer patients and differentially PCR selected against normal tissue can be bacterially displayed, as described above. In the same manner, antibody libraries displayed on bacteriophages, derived from normal patients or cancer patients, are allowed to interact with the cDNA displaying microorganisms and infection is again mediated by specific receptor-ligand interactions.

(3) cDNA derived from allergen encoding gene sequences can be bacterially displayed as described above. In the same manner, antibody libraries displayed on bacteriophages derived from normal or atopic patients are allowed to interact with the cDNA displaying microorganisms and infection is again mediated by specific receptor-ligand interactions.

Brief Description of the Drawings

Figure 1 shows a schematic illustration of the CLAP infection.

Figure 2 shows the infectivity by VCS M13 helper phages of E. coli carrying the plasmids (a) JFLO, (b) pTRAP and JCFLtraA1 and (c) pTRAPCMV and JCFLtraA1.

Figure 3 shows the infectivity of E. coli carrying the plasmids pTRAPCMV and JCFtraA1 by a specific phage stock (anti-CMV) and two non-specific phage stocks (anti-lys and anti-ox).

Detailed Description

Definitions

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As used herein "library" means a number of fragments of a ligand or receptor population, either their encoding sequences or their corresponding protein or peptide sequence displayed on a surface. Typically, libraries will

10 comprise a substantial number of such nucleic acid sequences or peptides. By way of example, libraries can be constructed after the principles outlined by Huse et al, 1989, Science, 246, 1275.

15

The expressions "ligand" and "receptor" refer to pairs of molecules or functional parts thereof, capable of specific binding to each other. Examples of such specific ligand-receptor pairs are: antibody-antigen, hormone-hormone receptor, growth factor-growth factor receptor, enzyme-

20 substrate and biotin-avidin etc.

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"Host microorganisms" include bacteria such as E. coli or other Gram negative bacteria, Gram positive bacteria, as well as unicellular microorganisms of eukaryotic origin

such as yeast.

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"Replicable genetic unit" comprises viruses and bacteriophages such as M13, fl and fd, but also bacteria, as well as unicellular microorganisms of eukaryote origin

such as yeast.

35

"Membrane passage DNA (mp-DNA)" are nucleic acid sequences encoding ligand or receptor molecules, or functional fragments thereof, this nucleic acid being initially

contained in a replicable genetic unit and being transferred to the host microorganism if binding of the displayed ligand/receptor pair takes place.

"Translocating determining DNA (td-DNA)" are nucleic acid sequences encoding ligand or receptor molecules, or functional fragments thereof, this nucleic acid being contained in a host microorganism and associated with sequences that mediate transfer of mp-DNA from a replicable genetic unit when displayed ligand and receptor molecules bind to each other.

The "surface molecule" will be dependent on the choice of host microorganism and replicable genetic unit. If the host organism is *E. coli*, suitable surface molecules can be selected from the group OmpA, lipoprotein, Lpp, IgA protease, LamB, fimbriae, flagellae or pilin. Pilin is preferred. Dependent on the choice of the replicable genetic unit, the surface molecule can be any surface molecule involved in the infection of, or in the transformation of DNA to, the host. Preferred replicable genetic units are filamentous bacteriophages such as fd and M13, suitable surface molecules of these phages can be protein III or protein VIII. Most preferred is protein III of the filamentous bacteriophage M13.

The "selection" of host organisms which have been infected, or otherwise transformed with DNA, is dependent on the fact that only host organism and replicable genetic unit pairs which have formed a receptor-ligand pair will infect each other.

Host organisms which have been infected, or in other ways transformed with DNA, can be "isolated" by the use of different selections markers such as different antibiotic resistance, e.g. ampicillin, tetracyclin or chloramphenicol, on different types of DNA.

"Determination" of the encoding sequences can be conducted with conventional DNA (or RNA) manual or automatic sequencer, according to known methods.

"Encoding sequence" can mean the corresponding DNA sequence of a protein or RNA or complementary DNA or RNA sequence thereof.

5

With "protein" means any sequence of amino acids including any peptide fragments thereof.

Examples

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The following examples are provided by way of illustration and are not intended to limit the scope of the invention. Those skilled in the art will be aware of alternative routine procedures that could be substituted for those described in the examples below.

15

Example 1

Vector constructions

20 (a) A vector (pTRAPchl^R) carrying the information for the pili molecule, pilin, of E. coli was constructed. The traA gene, encoding the pilin, was amplified by PCR from the plasmid pBF203 using:

25 5'-TCA CGG AAG CTT TCA TCA GAG GCC AAC GAC GGC CAT AC as the 3' primer; and,

5'-GTC GAC CTG CAG ACA GAG TTA TTG ATC ATT TGA TCA AGT TTC CTG ATT TTT A as the 5' primer.

30

The amplified fragment was cut with restriction enzymes Hind III/Pst I, purified and inserted into the Hind III/Pst I site of the plasmid pAM18chl^R. The new vector was called pTRAPchl^R and formed functional pili when co-transformed with an F episome called JCFLtraA1, which has a point mutation in the traA gene (see Achtman et al, J. Bacteriol., 106, 529-538, (1971)). The mutated episome

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contains all of the genes other than traA needed for the infection procedure, the traA being responsible for building up the pilin molecules.

5 pAM18chl^R vector was constructed by isolating the Hae II lacZ α peptide fragment from pUC18, treating with S1 nuclease and ligating into the "filled-in" Hind III/BamH I site of pACYC 184.

10 (b) A vector (pTRAPV3chl^R) was constructed that included nucleic acid encoding the pilin molecule, with an addition of nucleic acid sequence encoding a part of the V3 loop of HIV-1 (V3 is the variable loop of gp120 of HIV-1 (LA1)).
15 The nucleic acid encoding the V3 loop was arranged so that it would be expressed at the C-terminal end of the pilin molecule. This was achieved through PCR amplification of the traA gene from the plasmid pBF203, with a 5' primer as described above, and the following 3' primer: 5'-TCA CGG
20 AAG CTT TCA TCA AAC GAA AGC ACG ACC CGG ACC ACG CTG GAT ACG GAT AGA TTT ACG GAG GCC ACC GAC GGC CAT AC, which includes 45 bases coding for 15 amino acids of the V3 loop. This amplified fragment was inserted, as described above, in pAM18chl^R. This vector was called pTRAPV3chl^R.

25 (c) A vector (pTRAPCMVchl^R) was constructed that carries nucleic acid encoding a pilin molecule with the addition of the sequence of a part of the gB protein of CMV (cytomegalovirus). The nucleic acid encoding the gB
30 fragment was arranged so that it would be expressed at the C-terminal end of the pilin molecule. This was achieved through PCR amplification of the traA gene from the plasmid pBF203 with a 5' primer as described above, with the following 3' primer: 5'-TCA CGG AAG CTT TCA TCA TCC GTA CTT
35 GAG GGT AGT GTT GTA GAT AGT CTC GTT GGC GAG GCC AAC GAC GGC CAT AC, which includes 39 bases coding for 13 amino acids of the gB protein. This amplified fragment was inserted in

15

pAM18chl^R as described above. This vector was called pTRAPCMVchl^R.

Example 2

5 Vector construction

Construction of vectors containing nucleic acid encoding antigen fragments.

10 (a) A vector (pTRAPtet^R) carrying the information for the pili molecule, pilin, of E. coli was constructed. The traA gene, encoding the pilin, was amplified by PCR from the vector pTRAPchl^R (example 1) using:

15 5'-TCA CGG CCA TGG ATG CCG GCC ACG ATG CGT CCG
as 3' primer; and,

5'-GTC CAC CCA TGG CTC ATG TTT GAC AGC TTA TCA TC
as 5' primer.

20 The amplified fragment was cut with restriction enzyme NcoI, purified and inserted into the NcoI site of the plasmid pACYC184ΔHindIII. The new vector was called pTRAPtet^R and was capable of forming functional pili if co-
25 transformed with an F episome called pOX38A::CAT, which has a CAT cassette inserted into its traA gene to abolish its function.

30 pACYC184ΔHindIII was constructed by cutting the plasmid pACYC184 with HindIII, treatment with Klenow and religation, to abolish the unique HindIII site.

35 (b) A vector (pTRAPV3tet^R) was constructed that carries the information for the pilin molecule with an addition of the sequence of a part of the V3 loop of HIV-1 (V3 is the variable loop of gp120 of HIV-1 (LA1)) constructed to be expressed in the C-terminal end of the pilin molecule.

This was achieved through PCR amplification of the traA gene and the V3 peptide-coding sequence from the vector pTRAPV3chl^R, with the primers described in example 2a. This amplified fragment was inserted, as described above, in pACYC184ΔHindIII. This vector is called pTRAPV3tet^R.

(c) A vector (pTRAPCMVtet^R) was constructed that carries the information for the pilin molecule with an addition of the sequence of a part of the gB protein of CMV (cytomegalovirus), constructed to be expressed in the C-terminal end of the pilin molecule. This was achieved through PCR amplification of the traA gene and the CMV peptide-coding sequence from the vector pTRAPCMVchl^R, with the primers described in example 2a. This amplified fragment was inserted, as described above, in pACYC184ΔHindIII. This vector was called pTRAPCMVtet^R.

(d) A vector (pAM18tet^R) was constructed by PCR amplification of the pUC-insert from pAM18chl^R, containing a lacZ α peptide fragment, using primers as described in example 2a. This amplified fragment was inserted, as described above, in pACYC184ΔHindIII. This vector was called pAM18tet^R.

E. coli strain TG1 was used for the genetic constructions.

Example 3

Construction of filamentous bacteriophages displaying antibody fragments

The filamentous bacteriophage VCS M13 (helper phage) was obtained from Stratagene.

The M13 phages expressing Fab against the V3 loop of HIV (anti-V3), Fab against phenyl-oxazolone (anti-ox), Fab against hen egg lysozyme (anti-lys) and scFv against gB of CMV (anti-CMV), respectively, were prepared as follows:

XL1 Blue E. coli strain cells were transformed (according to Hanahan, 1983, J. Mol. Biol. 166, 557-580) with the vector pEXmide III (Söderlind et al, 1993, Bio/Technology 11, 503-507) carrying the VH and VL sequences of anti-V3, anti-ox and anti-lys, respectively, or with the vector pEXmide 4 (Ohlin, M., Owman, H., Mach, M. and Borrebaeck, C.A.K., 1996, "Light chain shuffling of a high affinity antibody results in a drift in epitope recognition.", Mol. Immunol., 33, 47-56, (1996)) carrying the VH and VL sequences for anti-CMV, and grown in ampicillin, tetracyclin and glucose containing LB media overnight in 37°C. The bacteria was reinoculated and grown to OD (600 nm) of 0.5, washed with LB and resuspended in LB, containing ampicillin and tetracyclin, and then superinfected with VCS M13 in the ratio 20 phages/cell. After growth for 1 hour in 37°C kanamycin was added and growth was continued overnight. The phage containing supernatant was recovered by centrifugation 8000 rpm for 10 minutes.

The phages obtained carry the antibody Fab fragments linked by the heavy chain constant domain to the N-terminal of protein III (pIII) or the antibody scFv fragments linked by the light chain variable domain to the N-terminal of pIII.

Example 4

Infection assays

To prove the function of the above mentioned genetic constructions three types of E. coli cells were established; (a) E. coli strain JC 3272, containing the unmutated F episome (JCFL0) (b) E. coli strain ED 2601, containing the F episome mutated in the traA gene (JCFLtraA1) and transformed with the pTRAP vector and (c) E. coli strain ED 2601, containing the F episome mutated in the traA gene (JCFLtraA1) and transformed with the pTRAPCMV vector.

The function of each type of *E. coli* was evaluated through its ability to express functional F pili and thus be infected with filamentous bacteriophages.

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Infections assays were carried out by incubating 100 μ l of *E. coli* with 10 μ l of phage stock at room temperature for 45 minutes, followed by plating on LB agar plates with the appropriate antibiotics (kanamycin for the helper phages and ampicillin for the specific phages, and chloramphenicol for the pTRAP constructs). The number of colony forming units, cfu, per plate were counted after overnight incubation in 37°C.

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The results are given in figures 2 and 3. Figure 2(a) shows that the wild type of VCS M13 expressing the pIII on the surface infects the F episome, JCFL0, containing *E. coli*. In 2(b) *E. coli* containing the F episome mutated in the *traA* gene, JCFLtraA1, and co-transformed with the pTRAP vector is infected by the VCS M13. This construct thus led to the formation of functional F pili, whereas the co-transformation with pTRAPCMV in figure 2(c) completely blocked with infection of wild type VCS M13 phage. Thus, a comparison of figure 2 (a) and (b) shows that the number of cfu obtained using the constructs of the invention (figure 2(b)) was comparable to the wt situation (figure 2(a)).

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Figure 3 shows the specificity of the infection. *E. coli* containing mutated F episome, JCFLtraA1, co-transformed with pTRAPCMV, form pili carrying the 13 amino acids peptide of gB of CMV. The anti-ox and anti-lys containing phages, expressing the anti-phenyl oxazolone or the anti-lysozyme antibody fragments connected to the pIII surface, did not infect the host carrying the gB of CMV on the pili due to lack of specificity. The antigen specific infection, mediated by 13 amino acid peptide of gB on the

pilin molecule, was clearly demonstrated by anti-CMV phages, which gave > 700 cfu/plate. Thus, inside the E. coli cells the two plasmids encoding gB peptide (ligand) and anti-CMV scFv (receptor) were physically linked by the
5 boundaries of the cell membrane.

The references mentioned above are all incorporated by reference.

CLAIMS:

1. A method for selecting nucleic acid sequences encoding ligand and receptor molecules capable of specific binding to each other, the method comprising:

5 (a) expressing in a host microorganism nucleic acid encoding a surface molecule which is operably linked to the expression of nucleic acid encoding a ligand or receptor molecule, or a functional fragments thereof, so that the
10 microorganism expresses the surface molecule and the ligand or receptor molecule as a fusion and displays it on its surface, wherein the host microorganism is modified so that it does not display the surface molecule other than as a fusion with the ligand or receptor molecule;

15 (b) contacting the modified host microorganism of step (a) with one or more replicable genetic units capable of expressing nucleic acid encoding ligand or receptor molecules, or functional fragments thereof, the ligand or receptor molecules being candidates for specific binding to
20 the molecules displayed by the host microorganisms of step (a) and being expressed as fusions with a surface protein of the replicable genetic unit, wherein binding of the surface displayed ligand and receptor molecules mediates the transfer of the nucleic acid encoding the ligand or
25 receptor from the replicable genetic unit to the microorganism; and,

(c) selecting the host microorganisms containing the nucleic acid sequences encoding the ligand and receptor molecules, or functional fragments thereof.

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2. A method for selecting specific ligand and receptor encoding sequences wherein:

35 (a) the expression of a surface molecule encoding sequence is combined with a ligand encoding sequence, or a sequence encoding a functional fragment thereof, so that the host microorganism expresses modified ligand molecules on its surface;

(b) infecting, or in other ways transferring DNA to, the modified host organism of step (a) with a genetically modified replicable genetic unit capable of expressing a receptor, or a functional fragment thereof, fused to a surface protein of the replicable genetic unit; and,

(c) selecting infected host organisms containing specific ligand and receptor encoding sequences or sequences encoding functional fragments thereof.

3. The method of claim 1 or claim 2 additionally comprising the step of:

(d) isolating the nucleic acid sequences encoding the ligand or receptor molecules.

4. The method of any one of claims 1 to 3 wherein the nucleic sequences encoding the ligand and/or receptor are associated with selection markers.

5. The method of any one of the preceding claims wherein the method is used to screen a library of microorganisms displaying different ligand or receptor molecules against libraries of replicable genetic units displaying candidate specific binding partners for the ligand or receptor molecules.

6. The method of any one of the preceding claims wherein the surface molecule encoding sequence of step (a) is combined with a receptor encoding sequence, or a functional fragment thereof, and the surface molecule encoding sequence of step (b) is fused to a ligand encoding sequence, or a functional fragment thereof.

7. The method of any one of the preceding claims wherein the host microorganism is modified to display the ligand or receptor by a bacterial display vector.

9. The method of any one of the preceding claims wherein the host microorganism is the bacteria *E. coli*.
10. The method of any one of the preceding claims wherein the surface molecule of the host organism is selected from the group OmpA, IgA protease or pilin.
11. The method of claim 10 wherein the surface molecule is pilin.
12. The method of any one of the preceding claims wherein the replicable genetic unit is a phage display vector.
13. The method of claim 12, wherein the phage display vector is a filamentous bacteriophage.
14. The method of claim 12 wherein the filamentous bacteriophage is fd, fl or M13.
15. The method of any one of the preceding claims wherein the surface molecule of the replicable genetic unit is pIII.
16. The method of any one of the preceding claims wherein the ligand is an antigen and the receptor is an antibody.
17. A kit for use in carrying out a method for selection of specific ligand and receptor encoding sequences as defined in any one of claim 1 to 16.
18. A kit for use in a method for selecting nucleic acid sequences encoding ligand and receptor molecules capable of specific binding to each other, the kit comprising:
- (a) a host microorganism modified so that it does not display a wild type surface protein;
 - (b) a vector encoding said surface protein and having restriction sites for the insertion of nucleic acid

encoding ligand or receptor molecules, or functional fragments thereof, so that when transformed into the host microorganism, the surface molecule and the ligand or receptor molecule are expressed as a fusion and displayed on the surface of the microorganism;

(c) a bacteriophage having a site for insertion of candidate binding partners to the ligand or receptor so that the binding partners are displayed on the surface of the bacteriophage as a fusion with a surface protein of the bacteriophage.

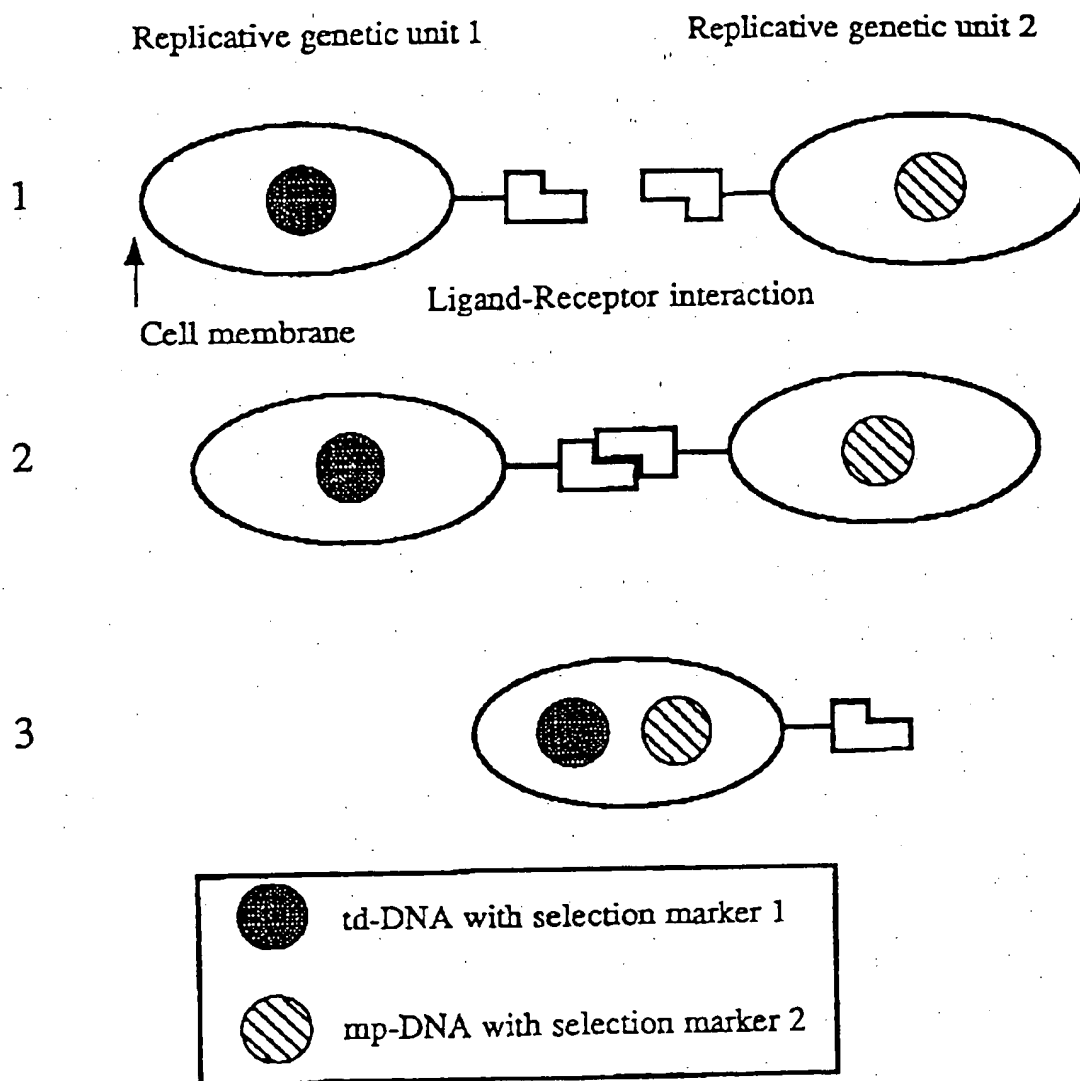


Figure 1

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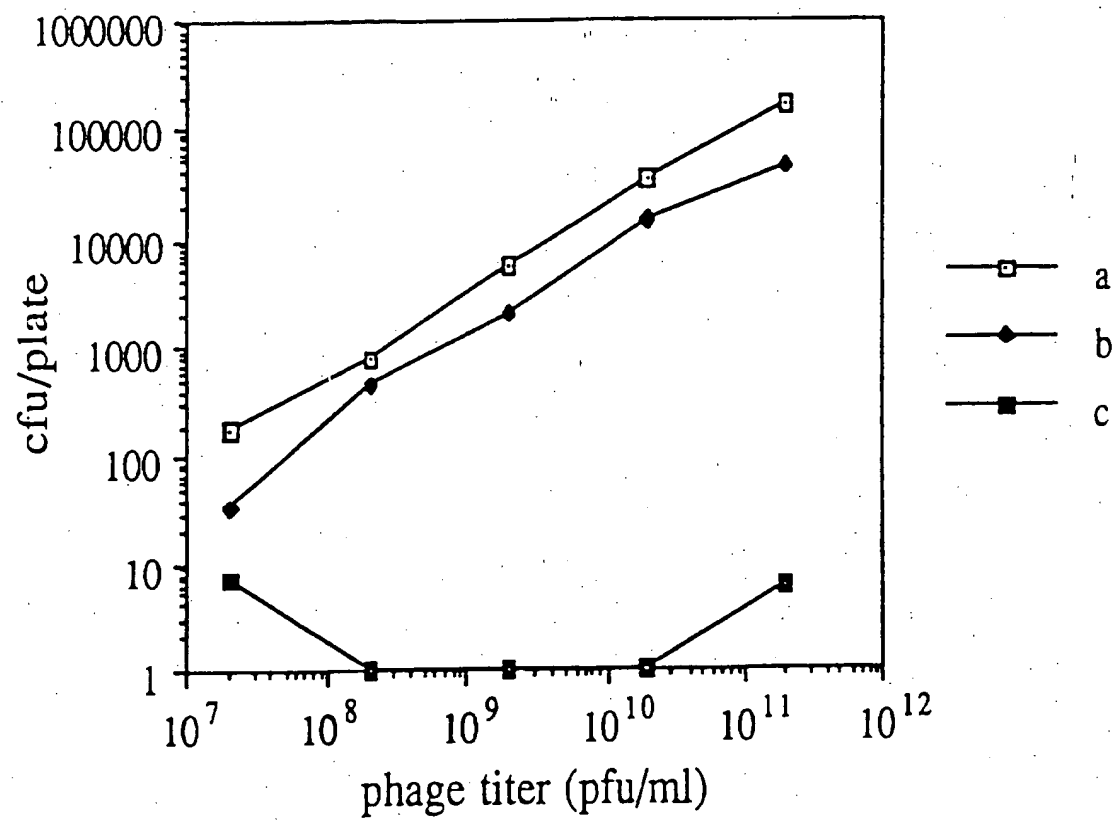


Figure 2

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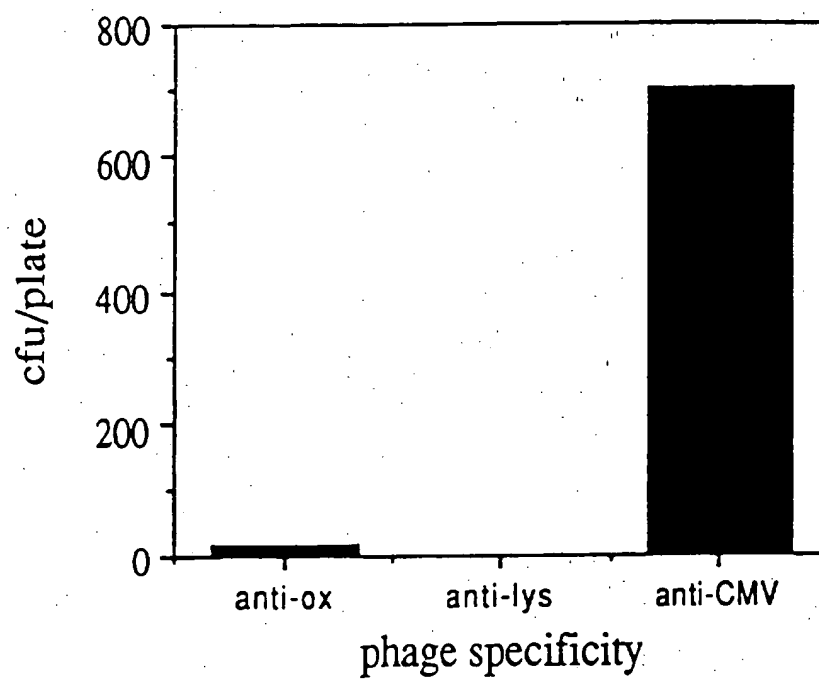


Figure 3

INTERNATIONAL SEARCH REPORT

International Application No
PL 1/GB 96/02271

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/10 C12N15/31 C12N15/38 C12N15/49 C12N15/62
C12N15/70 C12N1/21 C07K14/045 C07K14/16 C07K14/245

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EP,A,0 614 989 (MORPHOSYS GES FUER PROTEINOPTI) 14 September 1994 see the whole document ---	1-18
A	WO,A,95 16027 (BIOINVENT INT AB ;BORREBAECK CARL A K (SE); DUENAS MARTA (CU)) 15 June 1995 see the whole document ---	1-18
P,X	WO,A,95 34648 (DADE INT INC) 21 December 1995 see the whole document -----	1-6,9-17

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search

18 December 1996

Date of mailing of the international search report

21. 01. 97

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentaan 2
NL - 2280 HV Rijswijk
Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl,
Fax (+ 31-70) 340-3016

Authorized officer

Hornig, H

INTERNATIONAL SEARCH REPORT

International application No.

PCT/GB 96/02271

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 8
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
Claim 8 not included in the present application
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC./GB 96/02271

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP-A-0614989	14-09-94	CA-A- 2115811 DE-T- 614989 JP-A- 7039381 US-A- 5514548	18-08-94 28-09-95 10-02-95 07-05-96
WO-A-9516027	15-06-95	AU-A- 1252195 EP-A- 0739413	27-06-95 30-10-96
WO-A-9534648	21-12-95	US-A- 5516637 AU-A- 2828295 EP-A- 0722495	14-05-96 05-01-96 24-07-96